

SEQUENCE LISTING

<110> Thompson, John E.
 Wang, Tzann-Wei
 Lu, Dongen Lilly

<120> DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
 PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
 DEATH IN PLANTS

<130> 10799/9

<140>
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<150> 09/348,675
 <151> 1999-07-06

<160> 35

<170> PatentIn Ver. 2.1

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 <213> Lycopersicon sp.

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 <222> (54..1196)

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 Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
 5 10 15

ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc 152
 Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
 20 25 30

tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg 200
 Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
 35 40 45

gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att 248
 Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
 50 55 60 65

gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag 296
 Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
 70 75 80

gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc 344
 Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
 85 90 95

tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt 392
 Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val

100

105

110

aga gac act gtc cgc tac ctt gtt cag cac cgg atg gtt gat gtt gtg	440
Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val Val	
115 120 125	
gtt act aca gct ggt ggt att gaa gag gat ctc ata aag tgc ctc gca	488
Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala	
130 135 140 145	
cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg	536
Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser	
150 155 160	
aaa gga ttg aac cgt att ggt aac tta ttg gtt cct aat gac aac tac	584
Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr	
165 170 175	
tgc aaa ttt gag aat tgg atc atc cca gtt ttt gac caa atg tat gag	632
Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu	
180 185 190	
gag cag att aat gag aag gtt cta tgg aca cca tct aaa gtc att gct	680
Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala	
195 200 205	
cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct	728
Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp Ala	
210 215 220 225	
tac aag aac cgg att cct gtc ttc tgt cct ggc ttg acg gat gga tca	776
Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser	
230 235 240	
ctt ggt gac atg cta tac ttc cat tct ttc aaa aag ggt gat cca gat	824
Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp	
245 250 255	
aat cca gat ctt aat cct ggt cta gtc ata gac att gta gga gat att	872
Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile	
260 265 270	
agg gcc atg aat ggt gaa gct gtc cat gct ggt ttg agg aag aca gga	920
Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr Gly	
275 280 285	
atg att ata ctg ggt gga ggg ctg cct aag cac cat gtt tgc aat gcc	968
Met Ile Ile Leu Gly Gly Leu Pro Lys His His Val Cys Asn Ala	
290 295 300 305	
aat atg atg cgc aat ggt gca gat ttt gcc gtc ttc att aac acc gca	1016
Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr Ala	
310 315 320	
caa gag ttt gat ggt agt gac tct ggt gcc cgt cct gat gaa gct gta	1064
Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val	
325 330 335	
tca tgg gga aag ata cgt ggt ggt gcc aag act gtg aag gtg cat tgt	1112
Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His Cys	
340 345 350	
gat gca acc att gca ttt ccc ata tta gta gct gag aca ttt gca gct	1160
Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala	
355 360 365	

aag agt aag gaa ttc tcc cag ata agg tgc caa gtt tgaacattga Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val 370 375 380	1206
ggaagctgtc cttccgacca cacatatgaa ttgctagctt ttgaagccaa cttgctagtg tgcagcacca tttattctgc aaaactgact agagagcagg gtatattcct ctaccccgag ttagacgaca tcctgtatgg ttcaaattaa ttattttct ccccttcaca ccatgttatt tagttctctt cctcttcgaa agtgaagagc ttagatgttc ataggtttg aattatgtt gagggttggtg ataactgact agtcctctta ccatatacat aatgtatcct tgtactatga gattttgggt gtgtttgata ccaaggaaaa tggtttattt gaaaacaatt ggattttaa tttattttt cttgtttaaa aaaaaaaaaa aaaaaaaaaa aaa	1266 1326 1386 1446 1506 1566 1609

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<213> Lycopersicon sp.

<220>
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Gly Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser 35 40 45
Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala 50 55 60
Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr 65 70 75 80
Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val 85 90 95
Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly 100 105 110
Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val 115 120 125
Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu 130 135 140
Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg 145 150 155 160
Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn 165 170 175
Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr 180 185 190
Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile 195 200 205

Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
 210 215 220
 Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
 225 230 235 240
 Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
 245 250 255
 Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
 260 265 270
 Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
 275 280 285
 Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
 290 295 300
 Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
 305 310 315 320
 Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
 325 330 335
 Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
 340 345 350
 Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
 355 360 365
 Ala Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
 370 375 380

<210> 3
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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 <210> 4
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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 <210> 5
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 <212> DNA
 <213> Arabidopsis sp.

 <220>
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 <222> (68..265, 348..536, 624..842, 979..1065,
 1154..1258, 1575..1862)

DNA sequence

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aat gtg ttg tgg act cct tct aaa ctg tta gca cggttcc gga aaa gaa Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu 205 210 215	1026
atc aac aat gag agt tca tac ctt tat tgg gca tac aag gtatccaaa Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys 220 225 230	1075
ttttaacctt ttttagtttt taatcatcct gtgaggaact cggggattta aattttccgc	1135
ttcttgcgt gttttagatg aat att cca gta ttc tgc cca ggg tta aca Met Asn Ile Pro Val Phe Cys Pro Gly Leu Thr 235 240	1186
gat ggc tct ctt ggg gat atg ctg tat ttt cac tct ttt cgt acc tct Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg Thr Ser 245 250 255	1234
ggc ctc atc atc gat gta gta caa ggtacttctt ttactcaata agtcagtgtg Gly Leu Ile Ile Asp Val Val Gln 260 265	1288
ataaaatattc ctgctacatc tagtgcagga atattgtaac tagtagtgca ttgttagctt	1348
tccaaattcag caacggactt tactgttaatg tgatatatctaa aggttcaaac gggagctagg	1408
agaatagcat aggggcattc tgatttaggt ttggggcact gggtaagag tttagagaata	1468
ataatcttgt tagttgtta tcaaactctt tgatggtag tctcttggta atttgaattt	1528
tatcacagtg ttatggctt ttgaaccagt taatgtttta tgaaca gat atc aga Asp Ile Arg	1583
gct atg aac ggc gaa gct gtc cat gca aat cct aaa aag aca ggg atg Ala Met Asn Gly Ala Val His Ala Asn Pro Lys Lys Thr Gly Met 270 275 280 285	1631
ata atc ctt gga ggg ggc ttg cca aag cac cac ata tgt aat gcc aat Ile Ile Leu Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn 290 295 300	1679
atg atg cgc aat ggt gca gat tac gct gta ttt ata aac acc ggg caa Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln 305 310 315	1727
gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat gaa gcc gtg tct Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser 320 325 330	1775
tgg ggt aaa att agg ggt tct gct aaa acc gtt aag gtc tgc ttt tta Trp Gly Lys Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu 335 340 345	1823
att tct tca cat cct aat tta tat ctc act cag tgg ttt tgagtacata Ile Ser Ser His Pro Asn Leu Tyr Leu Thr Gln Trp Phe 350 355 360	1872
tttaatattt gatcattctt gcaggtatac tttgtatgcta ccatagcctt cccattgttgc	1932
gttgcagaaa catttgcac aaagagagac caaacctgtg agtctaaagac ttaagaactg	1992
actggcggtt ttggccatgg attcttaaag atcgttgctt tttgatttttta cactggagtg	2052
accatataaac actccacatt gatgtggctg tgacgcgaat tgtcttcttgc gaaattgtac	2112

tttagttct ctcaacctaa aatgatttgc agattgtgtt ttcgtttaaa acacaagagt	2172
ctttagtca ataatcctt gccttataaa attattcagt tccacaaca cattgtgatt	2232
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<210> 6
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 <212> PRT
 <213> *Arabidopsis* sp.

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Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met Leu Thr	
35 40 45	
Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val Val Asn	
50 55 60	
Gln Met Phe Glu Phe Val Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu	
65 70 75 80	
Thr Thr Val Ala Glu Asp Cys Ser Glu Glu Lys Asn Pro Ser Phe	
85 90 95	
Arg Glu Ser Val Lys Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu	
100 105 110	
Val Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His	
115 120 125	
Met Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp Leu	
130 135 140	
Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro Gly	
145 150 155 160	
Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val	
165 170 175	
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Phe	
180 185 190	
Asp Glu Met Leu Lys Glu Gln Lys Glu Glu Asn Val Leu Trp Thr Pro	
195 200 205	
Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu Ile Asn Asn Glu Ser Ser	
210 215 220	
Tyr Leu Tyr Trp Ala Tyr Lys Met Asn Ile Pro Val Phe Cys Pro Gly	
225 230 235 240	
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg	
245 250 255	
Thr Ser Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala Met Asn	
260 265 270	
Gly Glu Ala Val His Ala Asn Pro Lys Lys Thr Gly Met Ile Ile Leu	
275 280 285	

Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg
 290 295 300
 Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln Glu Phe Asp
 305 310 315 320
 Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys
 325 330 335
 Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser
 340 345 350
 His Pro Asn Leu Tyr Leu Thr Gln Trp Phe
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<210> 7
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 7
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<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 8
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<210> 9
 <211> 1660
 <212> DNA
 <213> Dianthus sp.

<220>
 <223> DHS

<220>
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 <222> (256)..(1374)

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 gtgttggtgt ttttgaagtt gttttgata agcagaaccc agttgtttta cactttacc 180
 attgaactac tgcaattcta aaactttgtt tacatttaa ttccatcaaa gattgagttc 240
 agcataggaa aaagg atg gag gat gct aat cat gat agt gtg gca tct gcg 291
 Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala
 1 5 10

cac tct gca gca ttc aaa aag tcg gag aat tta gag ggg aaa agc gtt 339
 His Ser Ala Ala Phe Lys Ser Glu Asn Leu Glu Gly Lys Ser Val

DC01 345180 v 1

15

20

25

aag att gag ggt tat gat ttt aat caa ggt gta aac tat tcc aaa ctc	387
Lys Ile Glu Gly Tyr Asp Phe Asn Gln Gly Val Asn Tyr Ser Lys Leu	
30 35 40	
ttg caa tct ttc gct tct aat ggg ttt caa gcc tcg aat ctt gga gat	435
Leu Gln Ser Phe Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp	
45 50 55 60	
gcc att gaa gta gtt aat cat atg cta gat tgg agt ctg gca gat gag	483
Ala Ile Glu Val Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu	
65 70 75	
gca cct gtg gac gat tgt agc gag gaa gag agg gat cct aaa ttc aga	531
Ala Pro Val Asp Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg	
80 85 90	
gaa tct gtg aag tgc aaa gtg ttc ttg ggc ttt act tca aat ctt att	579
Glu Ser Val Lys Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile	
95 100 105	
tcc tct ggt gtt cgt gac aca att cgg tat ctc gtg caa cat cat atg	627
Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met	
110 115 120	
gtt gac gtg ata gta acg aca acc gga ggt ata gaa gaa gat cta ata	675
Val Asp Val Ile Val Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile	
125 130 135 140	
aaa gga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt	723
Lys Gly Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe	
145 150 155	
gcc tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt	771
Ala Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly	
160 165 170	
aat ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc	819
Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile	
175 180 185	
att cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc	867
Ile Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile	
190 195 200	
tta tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac	915
Leu Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn	
205 210 215 220	
gat gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta	963
Asp Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val	
225 230 235	
ttt tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt	1011
Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe	
240 245 250	
cat tct ttt cgc aat ccg ggt tta atc gtc gat gtt gtg caa gat ata	1059
His Ser Phe Arg Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile	
255 260 265	
aga gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc	1107
Arg Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly	
270 275 280	

atg att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca 1155
Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala
285 290 295 300

aac atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac act gcc 1203
Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala
305 310 315

gaa gag ttt gac ggc agt gat tct ggt gct cgc ccc gat gag gct att 1251
Glu Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile
320 325 330

tca tgg ggc aaa att agc gga tct gct aag act gtg aag gtg cat tgt 1299
Ser Trp Gly Lys Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys
335 340 345

gat gcc acg ata gct ttc cct cta cta gtc gct gag aca ttt gca gca 1347
Asp Ala Thr Ile Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala
350 355 360

aaa aga gaa aaa gag agg aag agc tgt taaaactttt ttgattgttg 1394
Lys Arg Glu Lys Glu Arg Lys Ser Cys
365 370

aaaaatctgt gttataacaag tctcgaaatg catttttagta attgacttga tcttattcatt 1454
tcaatgtgtt atcttgaaa atgttggtaa tggaaacatct cacctttct atacaacatt 1514
gttcatccat tgtactccgt atcttgcataat ttggaaaaaa aaaaaccgtc tattgttacg 1574
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<212> PRT
<213> Dianthus sp.

<220>
<223> DHS

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35 40 45

Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Glu Val
50 55 60

Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu Ala Pro Val Asp
65 70 75 80

Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg Glu Ser Val Lys
85 90 95

Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile Ser Ser Gly Val
100 105 110

Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met Val Asp Val Ile

115	120	125
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130	135	140
Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu Pro Gly		
145	150	155
160		
Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val		
165	170	175
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Leu		
180	185	190
Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp Thr Pro		
195	200	205
Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu Ser Ser		
210	215	220
Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys Pro Gly		
225	230	235
240		
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg		
245	250	255
Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile Arg Ala Val Asn		
260	265	270
Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile Ile Leu		
275	280	285
Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg		
290	295	300
Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala Glu Glu Phe Asp		
305	310	315
320		
Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile Ser Trp Gly Lys		
325	330	335
Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile		
340	345	350
Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala Lys Arg Glu Lys		
355	360	365
Glu Arg Lys Ser Cys		
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<210> 11
<211> 780
<212> DNA
<213> *Lycopersicon* sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (43) .. (522)

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Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala Ser Lys Thr Phe	
5 10 15 20	
cca cag caa gct gga acc atc cgt aag aat ggt tac atc gtt atc aaa	150
Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val Ile Lys	
25 30 35	
ggc cgt ccc tgc aag gtt gtt gag gtc tcc act tca aaa act gga aaa	198
Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys	
40 45 50	
cac gga cat gct aaa tgt cac ttt gtg gca att gac att ttc aat gga	246
His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly	
55 60 65	
aag aaa ctg gaa gat atc gtt ccg tcc tcc cac aat tgt gat gtg cca	294
Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp Val Pro	
70 75 80	
cat gtt aac cgt acc gac tat cag ctg att gat atc tct gaa gat ggt	342
His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly	
85 90 95 100	
ttt gtc tca ctt ctt act gaa agt gga aac acc aag gat gac ctc agg	390
Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys Asp Asp Leu Arg	
105 110 115	
ctt ccc acc gat gaa aat ctg ctg aag cag gtt aaa gat ggg ttc cag	438
Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys Asp Gly Phe Gln	
120 125 130	
gaa gga aag gat ctt gtg gtg tct gtt atg tct gcg atg ggc gaa gag	486
Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly Glu Glu	
135 140 145	
cag att aac gcc gtt aag gat gtt ggt acc aag aat tagttatgtc	532
Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn	
150 155 160	
atggcagcat aatcaactgcc aaagcttaa gacattatca tattctaatg tggtactttg	592
atatacttag attataaact gtgttatttg cactgttcaa aacaaaagaa agaaaaactgc	652
tgttatggct agagaaaagta ttggcttga gctttgaca gcacagttga actatgtcaa	712
aattctactt tttttttttt gggtaaaata ctgctcgttt aatgtttgc aaaaaaaaaa	772
aaaaaaaaa	780

<210> 12
 <211> 160
 <212> PRT
 <213> Lycopersicon sp.

<220>
 <223> eif-5A

<400> 12
 Met Ser Asp Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala
 1 5 10 15
 Ser Lys Thr Phe Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr

	20	25	30
Ile Val Ile Lys Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser			
35	40		45
Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp			
50	55	60	
Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn			
65	70	75	80
Cys Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile			
85	90		95
Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys			
100	105		110
Asp Asp Leu Arg Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys			
115	120	125	
Asp Gly Phe Gln Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala			
130	135	140	
Met Gly Glu Glu Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn			
145	150	155	160

<210> 13
<211> 812
<212> DNA
<213> *Dianthus* sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (67) .. (546

<400> 13

ctcttttaca tcaatcgaaa aaaaattagg gttcttattt tagagtgaga ggcgaaaaat 60

cgaacg atg tcg gac gac gat cac cat ttc gag tca tcg gcc gac gcc 108
Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala
1 5 10

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gga gca tcc aag act tac cct caa caa gct ggt aca atc cgc aag agc 156
Gly Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser
   15          20          25          30

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ggc cac atc gtc atc aaa aat cgc cct tgc aag gtg gtt gag gtt tct 204
Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser
35          40          45

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acc tcc aag act ggc aag cac ggt cat gcc aaa tgt cac ttt gtt gcc 252
Thr Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala
      50          55          60

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att gac att ttc aac ggc aag aag ctg gaa gat att gtc ccc tca tcc 300
 Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser
 65 70 75

cac aat tgt gat gtt cca cat gtc aac cgt gtc gac tac cag ctg ctt 348
 His Asn Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu
 80 85 90

gat atc act gaa gat ggc ttt gtt agt ctg ctg act gac agt ggt gac 396
 Asp Ile Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp
 95 100 105 110

acc aag gat gat ctg aag ctt cct gct gat gag gcc ctt gtg aag cag 444
 Thr Lys Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln
 115 120 125

atg aag gag gga ttt gag gcg ggg aaa gac ttg att ctg tca gtc atg 492
 Met Lys Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met
 130 135 140

tgt gca atg gga gaa gag cag atc tgc gcc gtc aag gac gtt agt ggt 540
 Cys Ala Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly
 145 150 155

ggc aag tagaagcttt tcatgtatcc aatactacgc ggtgcagttt aagcaatagt 596
 Gly Lys
 160

aatctcgaga acattctgaa ccttatatgt tgaattgatg gtgccttagtt tgttttggaa 656
 atctcttgc aatataagttt taccaaatca atggatgtaa tgtcttgaat ttgttttattt 716
 tttgttttga tggttgcgtgt gattgcattt tgcattgtta tgagttatga cctgttataaa 776
 cacaagggttt tggtaaaaaaa aaaaaaaaaa aaaaaaa 812

<210> 14
 <211> 160
 <212> PRT
 <213> Dianthus sp.

<220>
 <223> eif-5A

<400> 14
 Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala Gly Ala
 1 5 10 15

Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser Gly His
 20 25 30

Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
 35 40 45

Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
 50 55 60

Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
 65 70 75 80

Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu Asp Ile
 85 90 95

Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp Thr Lys
 100 105 110

Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln Met Lys
 115 120 125

Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met Cys Ala
 130 135 140

Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly Gly Lys

145

150

155

160

<210> 15
 <211> 702
 <212> DNA
 <213> *Arabidopsis* sp.

<220>
 <223> eif-5A

<220>
 <221> CDS
 <222> (56)..(529)

<400> 15

ctgttaccaa aaaatctgta ccgcaaaatc ctcgtcgaag ctcgctgctg caacc atg 58
 Met
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tcc gac gag gag cat cac ttt gag tcc agt gac gcc gga gcg tcc aaa 106
 Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser Lys
 5 10 15

acc tac cct caa caa gct gga acc atc cgt aag aat ggt tac atc gtc 154
 Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val
 20 25 30

atc aaa aat cgt ccc tgc aag gtt gtt gag gtt tca acc tcg aag act 202
 Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr
 35 40 45

ggc aag cat ggt cat gct aaa tgt cat ttt gta gct att gat atc ttc 250
 Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe
 50 55 60 65

acc agc aag aaa ctc gaa gat att gtt cct tct tcc cac aat tgt gat 298
 Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp
 70 75 80

gtt cct cat gtc aac cgt act gat tat cag ctg att gac att tct gaa 346
 Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu
 85 90 95

gat gga tat gtc agt ttg ttg act gat aac ggt agt acc aag gat gac 394
 Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp Asp
 100 105 110

ctt aag ctc cct aat gat gac act ctg ctc caa cag atc aag agt ggg 442
 Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser Gly
 115 120 125

ttt gat gat gga aaa gat cta gtg gtg agt gta atg tca gct atg gga 490
 Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly
 130 135 140 145

gag gaa cag atc aat gct ctt aag gac atc ggt ccc aag tgagactaac 539
 Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
 150 155

aaagcctccc ctttgttatg agattcttct tcttctgttag gcttccattt ctcgtcggag 599

attatcttgt ttttgggtta ctcctatttt ggatatttaa acttttgtta ataatgccat 659

cttcttcaac ctttccttc tagatggttt ttatacttct tct 702

<210> 16
<211> 158
<212> PRT
<213> Arabidopsis sp.

<220>
<223> eif-5A

<400> 16
Met Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser
1 5 10 15
Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile
20 25 30
Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys
35 40 45
Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile
50 55 60
Phe Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys
65 70 75 80
Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser
85 90 95
Glu Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp
100 105 110
Asp Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser
115 120 125
Gly Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met
130 135 140
Gly Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
145 150 155

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
aaarrycgmc cytgcaagggt

20

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
aatacgactc actatacg

17

<210> 19	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<220>	
<223> "n" bases represent a, t, c, g, other or unknown	
<400> 19	20
tcytnccyt cmkctaahcc	
<210> 20	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 20	17
attaaccctc actaaag	
<210> 21	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 21	22
ctgttaccaa aaaatctgtta cc	
<210> 22	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 22	21
agaagaagta taaaaaccat c	
<210> 23	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 23	23
aaagaatcct agagagagaa agg	
<210> 24	
<211> 18	
<212> DNA	

DC01 345180 v 1

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 24
ttttacatca atcgaaaaa 18

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 25
accaaaaacct gtgttataac tcc 23

<210> 26
<211> 581
<212> DNA
<213> Arabidopsis sp.
<220>
<223> DHS
<220>
<221> CDS
<222> (1)..(579)
<400> 26
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Gly Gly Val Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
1 5 10 15
ggt gat ttc tct cta cct gga gct tat tta agg tca aag gga ttg aac 96
Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
20 25 30
cga att ggg aat ttg ctg gtt cct aat gat aac tac tgc aag ttt gag 144
Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
35 40 45
gat tgg atc att ccc atc ttt gac gag atg ttg aag gaa cag aaa gaa 192
Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
50 55 60
gag aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa 240
Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
65 70 75 80
gaa atc aac aat gag agt tca tac ctt tat tgg gca tac aag atg aat 288
Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
85 90 95
att cca gta ttc tgc cca ggg tta aca gat ggc tct ctt agg gat atg 336
Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
100 105 110
ctg tat ttt cac tct ttt cgt acc tct ggc ctc atc atc gat gta gta 384
Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
115 120 125

caa gat atc aga gct atg aac ggc gaa gct gtc cat gca aat cct aaa	432
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys	
130 135 140	
aag aca ggg atg ata atc ctt gga ggg ggc ttg cca aag cac cac ata	480
Lys Thr Gly Met Ile Ile Leu Gly Gly Leu Pro Lys His His Ile	
145 150 155 160	
tgt aat gcc aat atg atg cgc aat ggt gca gat tac gct gta ttt ata	528
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile	
165 170 175	
aac acc ggg caa gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat	576
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp	
180 185 190	
gaa gc	581
Glu	

<210> 27
 <211> 522
 <212> DNA
 <213> Dianthus sp.

<220>
 <223> DHS

<220>
 <221> CDS
 <222> (3)..(521)

<400> 27	
ga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt gcc	47
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala	
1 5 10 15	

tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt aat	95
Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn	
20 25 30	

ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc att	143
Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile	
35 40 45	

cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc tta	191
Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu	
50 55 60	

tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac gat	239
Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp	
65 70 75	

gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta ttt	287
Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe	
80 85 90 95	

tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt cat	335
Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His	
100 105 110	

tct ttt cgc aat ccg ggt tta atc atc gat gtt gtg caa gat ata aga	383
Ser Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg	
115 120 125	

gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc atg	431
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Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met
 130 135 140
 att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca aac 479
 Ile Ile Leu Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn
 145 150 155
 atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac acc g 522
 Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
 160 165 170

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 28
 ttgargaaaga tycatmaart gcct 24

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 29
 ccatcaaayt cytgkgcrgt gtt 23

<210> 30
 <211> 484
 <212> DNA
 <213> Arabidopsis sp.

<220>
 <223> DHS

<220>
 <221> CDS
 <222> (2)..(112)

<400> 30
 t gca cgc cct gat gaa gct gtg tct tgg ggt aaa att agg ggt tct gct 49
 Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
 1 5 10 15

aaa acc gtt aag gtc tgc ttt tta att tct tca cat cct aat tta tat 97
 Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
 20 25 30

ctc act cag tgg ttt tgagtacata tttaatattg gatcattctt gcaggtatac 152
 Leu Thr Gln Trp Phe
 35

tgtgatgcta ccatagcctt cccattgttg gttgcagaaa catttgccac aaagagagac 212
 caaacctgtg agtctaagac ttaagaactg actggtcgtt ttggccatgg attcttaaag 272
 atcgttgctt tttgattta cactggagtg accatataac actccacatt gatgtggctg 332

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tgacgcgaat tgtcttcttg cgaattgtac ttttagttct ctcacaccaa aatgattgc 392
agattgtgtt ttcgtttaaa acacaagagt cttgttagtca ataatcctt gccttataaa 452
attattcagt tccaacaaaa aaaaaaaaaa aa 484

<210> 31
<211> 559
<212> DNA
<213> *Lycopersicon* sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (1) .. (156)

<220>
<223> "n" bases represent a, t, c, g, other or unknown

<400> 31

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ggc gct cgt cct gat gaa gct gta tca tgg gga aag ata cgt ggt ggt 48
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
   1          5          10          15

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gcc aag act gtg aag gtg cat tgt gat gca acc att gca ttt ccc ata	96
Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile	
20 25 30	

tta gta gct gag aca ttt gca gct aag agt aag gaa ttc tcc cag ata	144	
Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile		
35	40	45

agg tgc caa gtt tgaacattga ggaagctgtc cttccgacca cacatatgaa 196
Arg Cys Gln Val
50

ttgcttagctt ttgaagccaa cttgcttagtg tgcagcacca tttattctgc aaaactgact 256
agagagcagg gatatattcct ctaccccgag ttagacgaca tcctgtatgg ttcaaattaa 316
ttattttct ccccttcaca ccatgttatt tagttctt cctcttcgaa agtgaagagc 376
tttagatgttc ataggtttg aattatgttg gaggttggtg ataactgact agtcctctta 436
ccatatacat aatgtatcct tgtactatga gattttgggt gtgttgata ccaaggaaaa 496
atgtttatTTT ggaaaacaat tggattttta atttaaaaaa aattgnttaa aaaaaaaaaa 556
aaa 559

<210> 32
<211> 193
<212> PRT
<213> *Arabidopsis* sp.

<220>
<223> DHS

<400> 32
Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
1 5 10 15

Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
 20 25 30
 Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
 35 40 45
 Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
 50 55 60
 Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
 65 70 75 80
 Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
 85 90 95
 Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
 100 105 110
 Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
 115 120 125
 Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys
 130 135 140
 Lys Thr Gly Met Ile Ile Leu Gly Gly Leu Pro Lys His His Ile
 145 150 155 160
 Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile
 165 170 175
 Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp
 180 185 190
 Glu

 <210> 33
 <211> 173
 <212> PRT
 <213> Dianthus sp.

 <220>
 <223> DHS

 <400> 33
 Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu
 1 5 10 15
 Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu
 20 25 30
 Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro
 35 40 45
 Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp
 50 55 60
 Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu
 65 70 75 80
 Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys
 85 90 95
 Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser
 100 105 110

Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala
115 120 125
Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile
130 135 140
Ile Leu Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met
145 150 155 160
Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
165 170

<210> 34
<211> 37
<212> PRT
<213> Arabidopsis sp.

<220>
<223> DHS

<400> 34
Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
1 5 10 15
Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
20 25 30
Leu Thr Gln Trp Phe
35

<210> 35
<211> 52
<212> PRT
<213> Lycopersicon sp.

<220>
<223> DHS

<400> 35
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
1 5 10 15
Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
20 25 30
Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
35 40 45
Arg Cys Gln Val
50